

1
SEQUENCE LISTING



<110> Smith, Richard
Dodd, Ian
Mossakowska, Danuta, Ewa, Irena

<120> CONJUGATES OF SOLUBLE PEPTIDIC COMPOUNDS WITH
MEMBRANE-BINDING AGENTS

<130> 088362/0112

<140> 09/214,913

<141> 1999-03-16

<150> 2260288

<151> 1997-07-08

<150> 9614871.3

<151> 1996-07-15

<160> 51

<170> PatentIn Ver. 2.1

<210> 1

<211> 37

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
Oligonucleotide used to anneal to oligonucleotide
of SEQ ID NO.2

<400> 1

gcaccgcagt gcatcatccc gaacaaatgc taataaa

37

<210> 2

<211> 37

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
Oligonucleotide used to anneal to oligonucleotide
of SEQ ID NO.1

<400> 2

agcttttatt agcatttggt cgggatgatg cactgcg

37

<210> 3

<211> 85

<212> DNA

<213> Artificial Sequence

of SEQ ID NO.4 to generate fragment 4

```
<400> 3
gcaccgcagt gcacatcccc gaacaaagac ggtccgaaaa agaagaaaaa gaaatctccg 60
tccaaatctt ccggttgcta ataaa                                     85
```

```
<210> 4
<211> 85
<212> DNA
<213> Artificial Sequence
```

```
<220>
<223> Description of Artificial Sequence:
      Oligonucleotide used to anneal to oligonucleotide
      of SEQ ID NO.3 to generate fragment 4
```

```
<400> 4
agctttttatt agcaaccgga agatttgac ggagatttct tttcttctt tttcggaccg 60
tctttgttcg ggatgatgca ctgcg                                     85
```

```
<210> 5
<211> 17
<212> PRT
<213> Artificial Sequence
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```
<220>
<221> UNSURE
<222> (17)
<223> NH2 group is linked to the C-terminal cysteine
```

```
<220>
<223> Description of Artificial Sequence: Peptide used
      to synthesie MSWP-1
```

```
<400> 5
Gly Ser Ser Lys Ser Pro Ser Lys Lys Lys Lys Lys Lys Pro Gly Asp
  1           5           10          15
```

Cys

```
<210> 6
<211> 198
<212> PRT
<213> Artificial Sequence
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```
<220>
<223> Description of Artificial Sequence: The petide
      sequence correpsonds to short consensus repeats
      1-3 of CR1 with a C-terminal cysteine
```

```
<400> 6
Met Gln Cys Asn Ala Pro Glu Trp Leu Pro Phe Ala Arg Pro Thr Asn
  1           5           10          15
```



Arg Asn Pro Pro Asp Pro Val Asn Gly Met Val His Val Ile Lys Gly
 65 70 75 80
 Ile Gln Phe Gly Ser Gln Ile Lys Tyr Ser Cys Thr Lys Gly Tyr Arg
 85 90 95
 Leu Ile Gly Ser Ser Ala Thr Cys Ile Ile Ser Gly Asp Thr Val
 100 105 110
 Ile Trp Asp Asn Glu Thr Pro Ile Cys Asp Arg Ile Pro Cys Gly Leu
 115 120 125
 Pro Pro Thr Ile Thr Asn Gly Asp Phe Ile Ser Thr Asn Arg Glu Asn
 130 135 140
 Phe His Tyr Gly Ser Val Val Thr Tyr Arg Cys Asn Pro Gly Ser Gly
 145 150 155 160
 Gly Arg Lys Val Phe Glu Leu Val Gly Glu Pro Ser Ile Tyr Cys Thr
 165 170 175
 Ser Asn Asp Asp Gln Val Gly Ile Trp Ser Gly Pro Ala Pro Gln Cys
 180 185 190
 Ile Ile Pro Asn Lys Asp Gly Pro Lys Lys Lys Lys Lys Lys Ser Pro
 195 200 205
 Ser Lys Ser Ser Gly Cys
 210

<210> 8
 <211> 215
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> UNSURE
 <222> (198)..(199)
 <223> Residues 1-198 are a first polypeptide chain and
 residues 199-215 are a second polypeptide chain
 linked by a disulphide bond formed between the
 cysteines at positions 198 and 199

<220>
 <221> UNSURE
 <222> (215)
 <223> The C-terminal glycine is linked to an
 N-(Myristoyl) group

<220>
 <221> UNSURE
 <222> (198)
 <223> The cysteine at position 198 is -Cys-COOH

<223> The cysteine at position 199 is CONH2-Cys-

<220>

<223> Description of Artificial Sequence:

[SCR1-3] -Cys-S-S- [MSWP-1]

<400> 8

Met	Gln	Cys	Asn	Ala	Pro	Glu	Trp	Leu	Pro	Phe	Ala	Arg	Pro	Thr	Asn
1				5				10						15	
Leu	Thr	Asp	Glu	Phe	Glu	Phe	Pro	Ile	Gly	Thr	Tyr	Leu	Asn	Tyr	Glu
		20						25					30		
Cys	Arg	Pro	Gly	Tyr	Ser	Gly	Arg	Pro	Phe	Ser	Ile	Ile	Cys	Leu	Lys
		35					40					45			
Asn	Ser	Val	Trp	Thr	Gly	Ala	Lys	Asp	Arg	Cys	Arg	Arg	Lys	Ser	Cys
	50					55					60				
Arg	Asn	Pro	Pro	Asp	Pro	Val	Asn	Gly	Met	Val	His	Val	Ile	Lys	Gly
	65				70				75					80	
Ile	Gln	Phe	Gly	Ser	Gln	Ile	Lys	Tyr	Ser	Cys	Thr	Lys	Gly	Tyr	Arg
			85				90						95		
Leu	Ile	Gly	Ser	Ser	Ala	Thr	Cys	Ile	Ile	Ser	Gly	Asp	Thr	Val	
		100					105					110			
Ile	Trp	Asp	Asn	Glu	Thr	Pro	Ile	Cys	Asp	Arg	Ile	Pro	Cys	Gly	Leu
	115					120					125				
Pro	Pro	Thr	Ile	Thr	Asn	Gly	Asp	Phe	Ile	Ser	Thr	Asn	Arg	Glu	Asn
	130					135					140				
Phe	His	Tyr	Gly	Ser	Val	Val	Thr	Tyr	Arg	Cys	Asn	Pro	Gly	Ser	Gly
	145				150					155				160	
Gly	Arg	Lys	Val	Phe	Glu	Leu	Val	Gly	Glu	Pro	Ser	Ile	Tyr	Cys	Thr
			165					170					175		
Ser	Asn	Asp	Asp	Gln	Val	Gly	Ile	Trp	Ser	Gly	Pro	Ala	Pro	Gln	Cys
		180					185					190			
Ile	Ile	Pro	Asn	Lys	Cys	Cys	Asp	Gly	Pro	Lys	Lys	Lys	Lys	Lys	Lys
	195						200					205			
Ser	Pro	Ser	Lys	Ser	Ser	Gly									
	210					215									

<210> 9

<211> 231

<212> PRT

<213> Artificial Sequence

<223> Residues 1-214 are a first polypeptide chain and residues 215-231 are a second polypeptide chain linked by a disulphide bond formed between the cysteines at positions 214 and 215

<220>

<221> UNSURE

<222> (231)

<223> The C-terminal glycine is linked to an N-[Myristoyl] group

<220>

<223> Description of Artificial Sequence: [SCR1-3/switch fusion] disulphide linked to [MSWP-1]

<220>

<221> UNSURE

<222> (214)

<223> The cysteine at position 214 is -Cys-COOH

<220>

<221> UNSURE

<222> (215)

<223> The cysteine at position 215 is CONH2-Cys-

<400> 9

Met	Gln	Cys	Asn	Ala	Pro	Glu	Trp	Leu	Pro	Phe	Ala	Arg	Pro	Thr	Asn
1				5				10						15	

Leu	Thr	Asp	Glu	Phe	Glu	Phe	Pro	Ile	Gly	Thr	Tyr	Leu	Asn	Tyr	Glu
		20						25					30		

Cys	Arg	Pro	Gly	Tyr	Ser	Gly	Arg	Pro	Phe	Ser	Ile	Ile	Cys	Leu	Lys
		35					40					45			

Asn	Ser	Val	Trp	Thr	Gly	Ala	Lys	Asp	Arg	Cys	Arg	Arg	Lys	Ser	Cys
	50					55					60				

Arg	Asn	Pro	Pro	Asp	Pro	Val	Asn	Gly	Met	Val	His	Val	Ile	Lys	Gly
65					70					75					80

Ile	Gln	Phe	Gly	Ser	Gln	Ile	Lys	Tyr	Ser	Cys	Thr	Lys	Gly	Tyr	Arg
				85					90					95	

Leu	Ile	Gly	Ser	Ser	Ser	Ala	Thr	Cys	Ile	Ile	Ser	Gly	Asp	Thr	Val
			100					105					110		

Ile	Trp	Asp	Asn	Glu	Thr	Pro	Ile	Cys	Asp	Arg	Ile	Pro	Cys	Gly	Leu
		115					120					125			

Pro	Pro	Thr	Ile	Thr	Asn	Gly	Asp	Phe	Ile	Ser	Thr	Asn	Arg	Glu	Asn
		130				135					140				

Phe	His	Tyr	Gly	Ser	Val	Val	Thr	Tyr	Arg	Cys	Asn	Pro	Gly	Ser	Gly
145					150					155					160

Ser Asn Asp Asp Gln Val Gly Ile Trp Ser Gly Pro Ala Pro Gln Cys
 180 185 190

Ile Ile Pro Asn Lys Asp Gly Pro Lys Lys Lys Lys Lys Lys Ser Pro
 195 200 205

Ser Lys Ser Ser Gly Cys Cys Asp Gly Pro Lys Lys Lys Lys Lys Lys
 210 215 220

Ser Pro Ser Lys Ser Ser Gly
 225 230

<210> 10
 <211> 1947
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> UNSURE
 <222> (1930)..(1931)
 <223> Residues 1-1930 are a first polypeptide chain and
 residues 1931-1947 are a second polypeptide chain
 linked by a disulphide bond formed between the
 cysteines at positions 1930 and 1931

<220>
 <221> UNSURE
 <222> (1947)
 <223> The C-terminal glycine is linked to an
 N-[Myristoyl] group

<220>
 <223> Description of Artificial Sequence: [CR1: 1-1929]
 - Cys-S-S-[MSWP-1]

<220>
 <221> UNSURE
 <222> (1930)
 <223> The cysteine at position 1930 is -Cys-COOH

<220>
 <221> UNSURE
 <222> (1931)
 <223> The Cysteine at position 1931 is CONH2-Cys-

<400> 10
 Gln Cys Asn Ala Pro Glu Trp Leu Pro Phe Ala Arg Pro Thr Asn Leu
 1 5 10 15

Thr Asp Glu Phe Glu Phe Pro Ile Gly Thr Tyr Leu Asn Tyr Glu Cys
 20 25 30

Arg Pro Gly Tyr Ser Gly Arg Pro Phe Ser Ile Ile Cys Leu Lys Asn

Ser Val Trp Thr Gly Ala Lys Asp Arg Cys Arg Arg Lys Ser Cys Arg
 50 55 60
 Asn Pro Pro Asp Pro Val Asn Gly Met Val His Val Ile Lys Gly Ile
 65 70 75 80
 Gln Phe Gly Ser Gln Ile Lys Tyr Ser Cys Thr Lys Gly Tyr Arg Leu
 85 90 95
 Ile Gly Ser Ser Ser Ala Thr Cys Ile Ile Ser Gly Asp Thr Val Ile
 100 105 110
 Trp Asp Asn Glu Thr Pro Ile Cys Asp Arg Ile Pro Cys Gly Leu Pro
 115 120 125
 Pro Thr Ile Thr Asn Gly Asp Phe Ile Ser Thr Asn Arg Glu Asn Phe
 130 135 140
 His Tyr Gly Ser Val Val Thr Tyr Arg Cys Asn Pro Gly Ser Gly Gly
 145 150 155 160
 Arg Lys Val Phe Glu Leu Val Gly Glu Pro Ser Ile Tyr Cys Thr Ser
 165 170 175
 Asn Asp Asp Gln Val Gly Ile Trp Ser Gly Pro Ala Pro Gln Cys Ile
 180 185 190
 Ile Pro Asn Lys Cys Thr Pro Pro Asn Val Glu Asn Gly Ile Leu Val
 195 200 205
 Ser Asp Asn Arg Ser Leu Phe Ser Leu Asn Glu Val Val Glu Phe Arg
 210 215 220
 Cys Gln Pro Gly Phe Val Met Lys Gly Pro Arg Arg Val Lys Cys Gln
 225 230 235 240
 Ala Leu Asn Lys Trp Glu Pro Glu Leu Pro Ser Cys Ser Arg Val Cys
 245 250 255
 Gln Pro Pro Pro Asp Val Leu His Ala Glu Arg Thr Gln Arg Asp Lys
 260 265 270
 Asp Asn Phe Ser Pro Gly Gln Glu Val Phe Tyr Ser Cys Glu Pro Gly
 275 280 285
 Tyr Asp Leu Arg Gly Ala Ala Ser Met Arg Cys Thr Pro Gln Gly Asp
 290 295 300
 Trp Ser Pro Ala Ala Pro Thr Cys Glu Val Lys Ser Cys Asp Asp Phe
 305 310 315 320
 Met Gly Gln Leu Leu Asn Gly Arg Val Leu Phe Pro Val Asn Leu Gln
 325 330 335
 Leu Gly Ala Lys Val Asp Phe Val Cys Asp Glu Gly Phe Gln Leu Lys

Gly Ser Ser Ala Ser Tyr Cys Val Leu Ala Gly Met Glu Ser Leu Trp
 355 360 365
 Asn Ser Ser Val Pro Val Cys Glu Gln Ile Phe Cys Pro Ser Pro Pro
 370 375 380
 Val Ile Pro Asn Gly Arg His Thr Gly Lys Pro Leu Glu Val Phe Pro
 385 390 395 400
 Phe Gly Lys Ala Val Asn Tyr Thr Cys Asp Pro His Pro Asp Arg Gly
 405 410 415
 Thr Ser Phe Asp Leu Ile Gly Glu Ser Thr Ile Arg Cys Thr Ser Asp
 420 425 430
 Pro Gln Gly Asn Gly Val Trp Ser Ser Pro Ala Pro Arg Cys Gly Ile
 435 440 445
 Leu Gly His Cys Gln Ala Pro Asp His Phe Leu Phe Ala Lys Leu Lys
 450 455 460
 Thr Gln Thr Asn Ala Ser Asp Phe Pro Ile Gly Thr Ser Leu Lys Tyr
 465 470 475 480
 Glu Cys Arg Pro Glu Tyr Tyr Gly Arg Pro Phe Ser Ile Thr Cys Leu
 485 490 495
 Asp Asn Leu Val Trp Ser Ser Pro Lys Asp Val Cys Lys Arg Lys Ser
 500 505 510
 Cys Lys Thr Pro Pro Asp Pro Val Asn Gly Met Val His Val Ile Thr
 515 520 525
 Asp Ile Gln Val Gly Ser Arg Ile Asn Tyr Ser Cys Thr Thr Gly His
 530 535 540
 Arg Leu Ile Gly His Ser Ser Ala Glu Cys Ile Leu Ser Gly Asn Ala
 545 550 555 560
 Ala His Trp Ser Thr Lys Pro Pro Ile Cys Gln Arg Ile Pro Cys Gly
 565 570 575
 Leu Pro Pro Thr Ile Ala Asn Gly Asp Phe Ile Ser Thr Asn Arg Glu
 580 585 590
 Asn Phe His Tyr Gly Ser Val Val Thr Tyr Arg Cys Asn Pro Gly Ser
 595 600 605
 Gly Gly Arg Lys Val Phe Glu Leu Val Gly Glu Pro Ser Ile Tyr Cys
 610 615 620
 Thr Ser Asn Asp Asp Gln Val Gly Ile Trp Ser Gly Pro Ala Pro Gln
 625 630 635 640
 Cys Ile Ile Pro Asn Lys Cys Thr Pro Pro Asn Val Glu Asn Gly Ile
 645 650 655

Leu Val Ser Asp Asn Arg Ser Leu Phe Ser Leu Asn Glu Val Val Glu
 660 665 670

Phe Arg Cys Gln Pro Gly Phe Val Met Lys Gly Pro Arg Arg Val Lys
 675 680 685

Cys Gln Ala Leu Asn Lys Trp Glu Pro Glu Leu Pro Ser Cys Ser Arg
 690 695 700

Val Cys Gln Pro Pro Pro Asp Val Leu His Ala Glu Arg Thr Gln Arg
 705 710 715 720

Asp Lys Asp Asn Phe Ser Pro Gly Gln Glu Val Phe Tyr Ser Cys Glu
 725 730 735

Pro Gly Tyr Asp Leu Arg Gly Ala Ala Ser Met Arg Cys Thr Pro Gln
 740 745 750

Gly Asp Trp Ser Pro Ala Ala Pro Thr Cys Glu Val Lys Ser Cys Asp
 755 760 765

Asp Phe Met Gly Gln Leu Leu Asn Gly Arg Val Leu Phe Pro Val Asn
 770 775 780

Leu Gln Leu Gly Ala Lys Val Asp Phe Val Cys Asp Glu Gly Phe Gln
 785 790 795 800

Leu Lys Gly Ser Ser Ala Ser Tyr Cys Val Leu Ala Gly Met Glu Ser
 805 810 815

Leu Trp Asn Ser Ser Val Pro Val Cys Glu Gln Ile Phe Cys Pro Ser
 820 825 830

Pro Pro Val Ile Pro Asn Gly Arg His Thr Gly Lys Pro Leu Glu Val
 835 840 845

Phe Pro Phe Gly Lys Ala Val Asn Tyr Thr Cys Asp Pro His Pro Asp
 850 855 860

Arg Gly Thr Ser Phe Asp Leu Ile Gly Glu Ser Thr Ile Arg Cys Thr
 865 870 875 880

Ser Asp Pro Gln Gly Asn Gly Val Trp Ser Ser Pro Ala Pro Arg Cys
 885 890 895

Gly Ile Leu Gly His Cys Gln Ala Pro Asp His Phe Leu Phe Ala Lys
 900 905 910

Leu Lys Thr Gln Thr Asn Ala Ser Asp Phe Pro Ile Gly Thr Ser Leu
 915 920 925

Lys Tyr Glu Cys Arg Pro Glu Tyr Tyr Gly Arg Pro Phe Ser Ile Thr
 930 935 940

Cys Leu Asp Asn Leu Val Trp Ser Ser Pro Lys Asp Val Cys Lys Arg

Lys Ser Cys Lys Thr Pro Pro Asp Pro Val Asn Gly Met Val His Val
 965 970 975
 Ile Thr Asp Ile Gln Val Gly Ser Arg Ile Asn Tyr Ser Cys Thr Thr
 980 985 990
 Gly His Arg Leu Ile Gly His Ser Ser Ala Glu Cys Ile Leu Ser Gly
 995 1000 1005
 Asn Thr Ala His Trp Ser Thr Lys Pro Pro Ile Cys Gln Arg Ile Pro
 1010 1015 1020
 Cys Gly Leu Pro Pro Thr Ile Ala Asn Gly Asp Phe Ile Ser Thr Asn
 1025 1030 1035 1040
 Arg Glu Asn Phe His Tyr Gly Ser Val Val Thr Tyr Arg Cys Asn Leu
 1045 1050 1055
 Gly Ser Arg Gly Arg Lys Val Phe Glu Leu Val Gly Glu Pro Ser Ile
 1060 1065 1070
 Tyr Cys Thr Ser Asn Asp Asp Gln Val Gly Ile Trp Ser Gly Pro Ala
 1075 1080 1085
 Pro Gln Cys Ile Ile Pro Asn Lys Cys Thr Pro Pro Asn Val Glu Asn
 1090 1095 1100
 Gly Ile Leu Val Ser Asp Asn Arg Ser Leu Phe Ser Leu Asn Glu Val
 1105 1110 1115 1120
 Val Glu Phe Arg Cys Gln Pro Gly Phe Val Met Lys Gly Pro Arg Arg
 1125 1130 1135
 Val Lys Cys Gln Ala Leu Asn Lys Trp Glu Pro Glu Leu Pro Ser Cys
 1140 1145 1150
 Ser Arg Val Cys Gln Pro Pro Pro Glu Ile Leu His Gly Glu His Thr
 1155 1160 1165
 Pro Ser His Gln Asp Asn Phe Ser Pro Gly Gln Glu Val Phe Tyr Ser
 1170 1175 1180
 Cys Glu Pro Gly Tyr Asp Leu Arg Gly Ala Ala Ser Leu His Cys Thr
 1185 1190 1195 1200
 Pro Gln Gly Asp Trp Ser Pro Glu Ala Pro Arg Cys Ala Val Lys Ser
 1205 1210 1215
 Cys Asp Asp Phe Leu Gly Gln Leu Pro His Gly Arg Val Leu Phe Pro
 1220 1225 1230
 Leu Asn Leu Gln Leu Gly Ala Lys Val Ser Phe Val Cys Asp Glu Gly
 1235 1240 1245
 Phe Arg Leu Lys Gly Ser Ser Val Ser His Cys Val Leu Val Gly Met

Arg Ser Leu Trp Asn Asn Ser Val Pro Val Cys Glu His Ile Phe Cys
 1265 1270 1275 1280
 Pro Asn Pro Pro Ala Ile Leu Asn Gly Arg His Thr Gly Thr Pro Ser
 1285 1290 1295
 Gly Asp Ile Pro Tyr Gly Lys Glu Ile Ser Tyr Thr Cys Asp Pro His
 1300 1305 1310
 Pro Asp Arg Gly Met Thr Phe Asn Leu Ile Gly Glu Ser Thr Ile Arg
 1315 1320 1325
 Cys Thr Ser Asp Pro His Gly Asn Gly Val Trp Ser Ser Pro Ala Pro
 1330 1335 1340
 Arg Cys Glu Leu Ser Val Arg Ala Gly His Cys Lys Thr Pro Glu Gln
 1345 1350 1355 1360
 Phe Pro Phe Ala Ser Pro Thr Ile Pro Ile Asn Asp Phe Glu Phe Pro
 1365 1370 1375
 Val Gly Thr Ser Leu Asn Tyr Glu Cys Arg Pro Gly Tyr Phe Gly Lys
 1380 1385 1390
 Met Phe Ser Ile Ser Cys Leu Glu Asn Leu Val Trp Ser Ser Val Glu
 1395 1400 1405
 Asp Asn Cys Arg Arg Lys Ser Cys Gly Pro Pro Pro Glu Pro Phe Asn
 1410 1415 1420
 Gly Met Val His Ile Asn Thr Asp Thr Gln Phe Gly Ser Thr Val Asn
 1425 1430 1435 1440
 Tyr Ser Cys Asn Glu Gly Phe Arg Leu Ile Gly Ser Pro Ser Thr Thr
 1445 1450 1455
 Cys Leu Val Ser Gly Asn Asn Val Thr Trp Asp Lys Lys Ala Pro Ile
 1460 1465 1470
 Cys Glu Ile Ile Ser Cys Glu Pro Pro Pro Thr Ile Ser Asn Gly Asp
 1475 1480 1485
 Phe Tyr Ser Asn Asn Arg Thr Ser Phe His Asn Gly Thr Val Val Thr
 1490 1495 1500
 Tyr Gln Cys His Thr Gly Pro Asp Gly Glu Gln Leu Phe Glu Leu Val
 1505 1510 1515 1520
 Gly Glu Arg Ser Ile Tyr Cys Thr Ser Lys Asp Asp Gln Val Gly Val
 1525 1530 1535
 Trp Ser Ser Pro Pro Pro Arg Cys Ile Ser Thr Asn Lys Cys Thr Ala
 1540 1545 1550
 Pro Glu Val Glu Asn Ala Ile Arg Val Pro Gly Asn Arg Ser Phe Phe

Ser Leu Thr Glu Ile Ile Arg Phe Arg Cys Gln Pro Gly Phe Val Met
 1570 1575 1580

Val Gly Ser His Thr Val Gln Cys Gln Thr Asn Gly Arg Trp Gly Pro
 1585 1590 1595 1600

Lys Leu Pro His Cys Ser Arg Val Cys Gln Pro Pro Pro Glu Ile Leu
 1605 1610 1615

His Gly Glu His Thr Leu Ser His Gln Asp Asn Phe Ser Pro Gly Gln
 1620 1625 1630

Glu Val Phe Tyr Ser Cys Glu Pro Ser Tyr Asp Leu Arg Gly Ala Ala
 1635 1640 1645

Ser Leu His Cys Thr Pro Gln Gly Asp Trp Ser Pro Glu Ala Pro Arg
 1650 1655 1660

Cys Thr Val Lys Ser Cys Asp Asp Phe Leu Gly Gln Leu Pro His Gly
 1665 1670 1675 1680

Arg Val Leu Leu Pro Leu Asn Leu Gln Leu Gly Ala Lys Val Ser Phe
 1685 1690 1695

Val Cys Asp Glu Gly Phe Arg Leu Lys Gly Arg Ser Ala Ser His Cys
 1700 1705 1710

Val Leu Ala Gly Met Lys Ala Leu Trp Asn Ser Ser Val Pro Val Cys
 1715 1720 1725

Glu Gln Ile Phe Cys Pro Asn Pro Pro Ala Ile Leu Asn Gly Arg His
 1730 1735 1740

Thr Gly Thr Pro Phe Gly Asp Ile Pro Tyr Gly Lys Glu Ile Ser Tyr
 1745 1750 1755 1760

Ala Cys Asp Thr His Pro Asp Arg Gly Met Thr Phe Asn Leu Ile Gly
 1765 1770 1775

Glu Ser Ser Ile Arg Cys Thr Ser Asp Pro Gln Gly Asn Gly Val Trp
 1780 1785 1790

Ser Ser Pro Ala Pro Arg Cys Glu Leu Ser Val Pro Ala Ala Cys Pro
 1795 1800 1805

His Pro Pro Lys Ile Gln Asn Gly His Tyr Ile Gly Gly His Val Ser
 1810 1815 1820

Leu Tyr Leu Pro Gly Met Thr Ile Ser Tyr Thr Cys Asp Pro Gly Tyr
 1825 1830 1835 1840

Leu Leu Val Gly Lys Gly Phe Ile Phe Cys Thr Asp Gln Gly Ile Trp
 1845 1850 1855

Ser Gln Leu Asp His Tyr Cys Lys Glu Val Asn Cys Ser Phe Pro Leu

Phe Met Asn Gly Ile Ser Lys Glu Leu Glu Met Lys Lys Val Tyr His
 1875 1880 1885

Tyr Gly Asp Tyr Val Thr Leu Lys Cys Glu Asp Gly Tyr Thr Leu Glu
 1890 1895 1900

Gly Ser Pro Trp Ser Gln Cys Gln Ala Asp Asp Arg Trp Asp Pro Pro
 1905 1910 1915 1920

Leu Ala Lys Cys Thr Ser Arg Ala His Cys Cys Asp Gly Pro Lys Lys
 1925 1930 1935

Lys Lys Lys Lys Ser Pro Ser Lys Ser Ser Gly
 1940 1945

<210> 11
 <211> 215
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> UNSURE
 <222> (198)..(199)
 <223> Residues 1-198 are a first polypeptide chain and
 residues 199-215 are a second polypeptide chain
 linked by a disulphide bond formed between the
 cysteines at positions 198 and 199

<220>
 <221> UNSURE
 <222> (199)
 <223> The cysteine at position 199 is linked to a
 NHCOCH3 group

<220>
 <221> UNSURE
 <222> (215)
 <223> The C-terminal lysine is is linked to an
 N-[Myristoyl]-NH2 group

<220>
 <223> Description of Artificial Sequence:
 [SCR1-3]-Cys-S-S-[MSWP-2]

<400> 11
 Met Gln Cys Asn Ala Pro Glu Trp Leu Pro Phe Ala Arg Pro Thr Asn
 1 5 10 15

Leu Thr Asp Glu Phe Glu Phe Pro Ile Gly Thr Tyr Leu Asn Tyr Glu
 20 25 30

Cys Arg Pro Gly Tyr Ser Gly Arg Pro Phe Ser Ile Ile Cys Leu Lys
 35 40 45

Arg Asn Pro Pro Asp Pro Val Asn Gly Met Val His Val Ile Lys Gly
 65 70 75 80
 Ile Gln Phe Gly Ser Gln Ile Lys Tyr Ser Cys Thr Lys Gly Tyr Arg
 85 90 95
 Leu Ile Gly Ser Ser Ser Ala Thr Cys Ile Ile Ser Gly Asp Thr Val
 100 105 110
 Ile Trp Asp Asn Glu Thr Pro Ile Cys Asp Arg Ile Pro Cys Gly Leu
 115 120 125
 Pro Pro Thr Ile Thr Asn Gly Asp Phe Ile Ser Thr Asn Arg Glu Asn
 130 135 140
 Phe His Tyr Gly Ser Val Val Thr Tyr Arg Cys Asn Pro Gly Ser Gly
 145 150 155 160
 Gly Arg Lys Val Phe Glu Leu Val Gly Glu Pro Ser Ile Tyr Cys Thr
 165 170 175
 Ser Asn Asp Asp Gln Val Gly Ile Trp Ser Gly Pro Ala Pro Gln Cys
 180 185 190
 Ile Ile Pro Asn Lys Cys Cys Asp Gly Pro Lys Lys Lys Lys Lys Lys
 195 200 205
 Ser Pro Ser Lys Ser Ser Lys
 210 215

<210> 12

<211> 213

<212> PRT

<213> Artificial Sequence

<220>

<221> UNSURE

<222> (198)..(199)

<223> Residues 1-198 are a first polypeptide chain and residues 199-213 are a second polypeptide chain linked by a disulphide bond formed between the cysteines at positions 198 and 199

<220>

<221> UNSURE

<222> (199)

<223> The cysteine at position 199 is linked to a CONH2 group

<220>

<221> UNSURE

<222> (213)

<223> The C-terminal serine is linked to an NH-[Myristoyl] group

[SCR1-3]-Cys-S-S-[MSWP-3]

<400> 12

Met	Gln	Cys	Asn	Ala	Pro	Glu	Trp	Leu	Pro	Phe	Ala	Arg	Pro	Thr	Asn
1				5					10					15	

Leu	Thr	Asp	Glu	Phe	Glu	Phe	Pro	Ile	Gly	Thr	Tyr	Leu	Asn	Tyr	Glu
		20						25					30		

Cys	Arg	Pro	Gly	Tyr	Ser	Gly	Arg	Pro	Phe	Ser	Ile	Ile	Cys	Leu	Lys
		35					40					45			

Asn	Ser	Val	Trp	Thr	Gly	Ala	Lys	Asp	Arg	Cys	Arg	Arg	Lys	Ser	Cys
	50					55					60				

Arg	Asn	Pro	Pro	Asp	Pro	Val	Asn	Gly	Met	Val	His	Val	Ile	Lys	Gly
65					70					75				80	

Ile	Gln	Phe	Gly	Ser	Gln	Ile	Lys	Tyr	Ser	Cys	Thr	Lys	Gly	Tyr	Arg
				85					90					95	

Leu	Ile	Gly	Ser	Ser	Ser	Ala	Thr	Cys	Ile	Ile	Ser	Gly	Asp	Thr	Val
		100						105					110		

Ile	Trp	Asp	Asn	Glu	Thr	Pro	Ile	Cys	Asp	Arg	Ile	Pro	Cys	Gly	Leu
		115					120					125			

Pro	Pro	Thr	Ile	Thr	Asn	Gly	Asp	Phe	Ile	Ser	Thr	Asn	Arg	Glu	Asn
		130				135					140				

Phe	His	Tyr	Gly	Ser	Val	Val	Thr	Tyr	Arg	Cys	Asn	Pro	Gly	Ser	Gly
145					150					155				160	

Gly	Arg	Lys	Val	Phe	Glu	Leu	Val	Gly	Glu	Pro	Ser	Ile	Tyr	Cys	Thr
			165					170					175		

Ser	Asn	Asp	Asp	Gln	Val	Gly	Ile	Trp	Ser	Gly	Pro	Ala	Pro	Gln	Cys
		180						185				190			

Ile	Ile	Pro	Asn	Lys	Cys	Cys	Lys	Thr	Lys	Ser	Lys	Lys	Lys	Lys	Lys
		195					200					205			

Lys	Gly	Asp	Lys	Ser
210				

<210> 13

<211> 214

<212> PRT

<213> Artificial Sequence

<220>

<221> UNSURE

<222> (198)..(199)

<223> Residues 1-198 are a first polypeptide chain and

<220>

<221> UNSURE

<222> (199)

<223> The cysteine at position 199 is linked to an
NHCOCH₃ group

<220>

<221> UNSURE

<222> (214)

<223> The C-terminal valine is linked to an -NH(CH₂)₉CH₃
group.

<220>

<223> Description of Artificial Sequence:

[SCR1-3]-Cys-S-S-[TCPT-1]

<400> 13

Met	Gln	Cys	Asn	Ala	Pro	Glu	Trp	Leu	Pro	Phe	Ala	Arg	Pro	Thr	Asn
1				5				10						15	

Leu	Thr	Asp	Glu	Phe	Glu	Phe	Pro	Ile	Gly	Thr	Tyr	Leu	Asn	Tyr	Glu
		20						25					30		

Cys	Arg	Pro	Gly	Tyr	Ser	Gly	Arg	Pro	Phe	Ser	Ile	Ile	Cys	Leu	Lys
		35					40					45			

Asn	Ser	Val	Trp	Thr	Gly	Ala	Lys	Asp	Arg	Cys	Arg	Arg	Lys	Ser	Cys
	50					55					60				

Arg	Asn	Pro	Pro	Asp	Pro	Val	Asn	Gly	Met	Val	His	Val	Ile	Lys	Gly
65					70					75					80

Ile	Gln	Phe	Gly	Ser	Gln	Ile	Lys	Tyr	Ser	Cys	Thr	Lys	Gly	Tyr	Arg
			85					90						95	

Leu	Ile	Gly	Ser	Ser	Ala	Thr	Cys	Ile	Ile	Ser	Gly	Asp	Thr	Val	
		100					105					110			

Ile	Trp	Asp	Asn	Glu	Thr	Pro	Ile	Cys	Asp	Arg	Ile	Pro	Cys	Gly	Leu
		115					120					125			

Pro	Pro	Thr	Ile	Thr	Asn	Gly	Asp	Phe	Ile	Ser	Thr	Asn	Arg	Glu	Asn
		130				135					140				

Phe	His	Tyr	Gly	Ser	Val	Val	Thr	Tyr	Arg	Cys	Asn	Pro	Gly	Ser	Gly
145					150					155					160

Gly	Arg	Lys	Val	Phe	Glu	Leu	Val	Gly	Glu	Pro	Ser	Ile	Tyr	Cys	Thr
			165					170						175	

Ser	Asn	Asp	Asp	Gln	Val	Gly	Ile	Trp	Ser	Gly	Pro	Ala	Pro	Gln	Cys
			180					185					190		

Ile	Ile	Pro	Asn	Lys	Cys	Cys	Ser	Ala	Ala	Pro	Ser	Ser	Gly	Phe	Arg
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

Ile Leu Leu Leu Lys Val
210

<210> 14
<211> 209
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: SCR1-3 with
the C-terminal amino acids N195 and K196 replaced
by a 14 amino acid peptide.

<400> 14
Met Gln Cys Asn Ala Pro Glu Trp Leu Pro Phe Ala Arg Pro Thr Asn
1 5 10 15
Leu Thr Asp Glu Phe Glu Phe Pro Ile Gly Thr Tyr Leu Asn Tyr Glu
20 25 30
Cys Arg Pro Gly Tyr Ser Gly Arg Pro Phe Ser Ile Ile Cys Leu Lys
35 40 45
Asn Ser Val Trp Thr Gly Ala Lys Asp Arg Cys Arg Arg Lys Ser Cys
50 55 60
Arg Asn Pro Pro Asp Pro Val Asn Gly Met Val His Val Ile Lys Gly
65 70 75 80
Ile Gln Phe Gly Ser Gln Ile Lys Tyr Ser Cys Thr Lys Gly Tyr Arg
85 90 95
Leu Ile Gly Ser Ser Ala Thr Cys Ile Ile Ser Gly Asp Thr Val
100 105 110
Ile Trp Asp Asn Glu Thr Pro Ile Cys Asp Arg Ile Pro Cys Gly Leu
115 120 125
Pro Pro Thr Ile Thr Asn Gly Asp Phe Ile Ser Thr Asn Arg Glu Asn
130 135 140
Phe His Tyr Gly Ser Val Val Thr Tyr Arg Cys Asn Pro Gly Ser Gly
145 150 155 160
Gly Arg Lys Val Phe Glu Leu Val Gly Glu Pro Ser Ile Tyr Cys Thr
165 170 175
Ser Asn Asp Asp Gln Val Gly Ile Trp Ser Gly Pro Ala Pro Gln Cys
180 185 190
Ile Ile Pro Thr Asn Ala Asn Lys Ser Leu Ser Ser Ile Ser Cys Gln
195 200 205
Thr

<210> 15
 <211> 53
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:
 Oligonucleotide used to generate a novel
 restriction site and a C-terminal cysteine in
 plasmid pBC04-29

 <400> 15
 ctggagcggg ccgcacccgc agtgcacat cccgaacaaa tgctaataaa agc 53

 <210> 16
 <211> 53
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:
 Oligonucleotide used to generate a novel
 restriction site and C terminal cysteine residue
 in plasmid pBC04-29

 <400> 16
 gcttttatta gcatttggtc gggatgatgc actgcggtgc gggcccgctc cag 53

 <210> 17
 <211> 224
 <212> PRT
 <213> Artificial Sequence

 <220>
 <221> UNSURE
 <222> (1)..(209)
 <223> Positions 1-209 are a first polypeptide chain
 which is linked to a second polypeptide chain
 (positions 210-224) by a disulphide linkage
 between the cysteines at positions 207 and 210.

 <220>
 <221> UNSURE
 <222> (210)
 <223> The cysteine at position 210 is linked to a -CONH2
 group

 <220>
 <221> UNSURE
 <222> (224)
 <223> The glycine at position 224 is linked to an
 -NH-[Myristoyl] group

 <220>
 <223> Description of Artificial Sequence:
 [SCP1-3/delN195-K206]LTWAKVSSSSG

<400> 17

Met Gln Cys Asn Ala Pro Glu Trp Leu Pro Phe Ala Arg Pro Thr Asn
 1 5 10 15

Leu Thr Asp Glu Phe Glu Phe Pro Ile Gly Thr Tyr Leu Asn Tyr Glu
 20 25 30

Cys Arg Pro Gly Tyr Ser Gly Arg Pro Phe Ser Ile Ile Cys Leu Lys
 35 40 45

Asn Ser Val Trp Thr Gly Ala Lys Asp Arg Cys Arg Arg Lys Ser Cys
 50 55 60

Arg Asn Pro Pro Asp Pro Val Asn Gly Met Val His Val Ile Lys Gly
 65 70 75 80

Ile Gln Phe Gly Ser Gln Ile Lys Tyr Ser Cys Thr Lys Gly Tyr Arg
 85 90 95

Leu Ile Gly Ser Ser Ser Ala Thr Cys Ile Ile Ser Gly Asp Thr Val
 100 105 110

Ile Trp Asp Asn Glu Thr Pro Ile Cys Asp Arg Ile Pro Cys Gly Leu
 115 120 125

Pro Pro Thr Ile Thr Asn Gly Asp Phe Ile Ser Thr Asn Arg Glu Asn
 130 135 140

Phe His Tyr Gly Ser Val Val Thr Tyr Arg Cys Asn Pro Gly Ser Gly
 145 150 155 160

Gly Arg Lys Val Phe Glu Leu Val Gly Glu Pro Ser Ile Tyr Cys Thr
 165 170 175

Ser Asn Asp Asp Gln Val Gly Ile Trp Ser Gly Pro Ala Pro Gln Cys
 180 185 190

Ile Ile Pro Thr Asn Ala Asn Lys Ser Leu Ser Ser Ile Ser Cys Gln
 195 200 205

Thr Cys Asp Gly Pro Lys Lys Lys Lys Lys Ser Lys Ser Ser Gly
 210 215 220

<210> 18

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<221> UNSURE

<222> (17)

<223> The C-terminal lysine is linked to an -NH₂ group

<220>

<223> Description of Artificial Sequence: Part 1a

<400> 18

Cys Asp Gly Pro Lys Lys Lys Lys Lys Lys Ser Pro Ser Lys Ser Ser
 1 5 10 15

Lys

<210> 19

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Peptide used
 to generate SEQ ID NO.29

<400> 19

Ser Lys Asp Gly Lys Lys Lys Lys Lys Lys Ser Lys Thr Lys Cys
 1 5 10 15

<210> 20

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Peptide used
 to generate SEQ ID NO.30

<400> 20

Cys Ser Ala Ala Pro Ser Ser Gly Phe Arg Ile Leu Leu Leu Lys Val
 1 5 10 15

<210> 21

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<221> UNSURE

<222> (1)

<223> The N-terminal glycine is linked to an
 N-[Myristoyl]- group

<220>

<221> UNSURE

<222> (17)

<223> The C-terminal cysteine is linked to
 -S-S-[4-butyrimino]-N-epsilon(Lys) [Streptokinase]

<220>

<221> UNSURE

<220>

<223> Description of Artificial Sequence: Conjugate of Streptokinase and MSWP-1

<400> 21

Gly Ser Ser Lys Ser Pro Ser Lys Lys Lys Lys Lys Lys Pro Gly Asp
1 5 10 15

Cys

<210> 22

<211> 527

<212> PRT

<213> Artificial Sequence

<220>

<221> UNSURE

<222> (478)

<223> Serine 478 is modified to:

O-4-CO-benzyl-NH(CH₂)₂NHCO(CH₂)₂-S-S-{Cys(-CONH₂)-
Asp-Gly-Pro-Lys-Lys-Lys-Lys-Lys-Ser-Pro-Ser-Ly
s-Ser-Ser-Gly}-~NH-[Myristoyl]

<220>

<223> Description of Artificial Sequence: Reversible linkage of MSWP-1 to the active centre of Human Tissue-type Plasminogen Activator

<400> 22

Ser Tyr Gln Val Ile Cys Arg Asp Glu Lys Thr Gln Met Ile Tyr Gln
1 5 10 15

Gln His Gln Ser Trp Leu Arg Pro Val Leu Arg Ser Asn Arg Val Glu
20 25 30

Tyr Cys Trp Cys Asn Ser Gly Arg Ala Gln Cys His Ser Val Pro Val
35 40 45

Lys Ser Cys Ser Glu Pro Arg Cys Phe Asn Gly Gly Thr Cys Gln Gln
50 55 60

Ala Leu Tyr Phe Ser Asp Phe Val Cys Gln Cys Pro Glu Gly Phe Ala
65 70 75 80

Gly Lys Cys Cys Glu Ile Asp Thr Arg Ala Thr Cys Tyr Glu Asp Gln
85 90 95

Gly Ile Ser Tyr Arg Gly Thr Trp Ser Thr Ala Glu Ser Gly Ala Glu
100 105 110

Cys Thr Asn Trp Asn Ser Ser Ala Leu Ala Gln Lys Pro Tyr Ser Gly
115 120 125

Arg	Asn	Pro	Asp	Arg	Asp	Ser	Lys	Pro	Trp	Cys	Tyr	Val	Phe	Lys	Ala	145	150	155	160
Gly	Lys	Tyr	Ser	Ser	Glu	Phe	Cys	Ser	Thr	Pro	Ala	Cys	Ser	Glu	Gly	165	170	175	
Asn	Ser	Asp	Cys	Tyr	Phe	Gly	Asn	Gly	Ser	Ala	Tyr	Arg	Gly	Thr	His	180	185	190	
Ser	Leu	Thr	Glu	Ser	Gly	Ala	Ser	Cys	Leu	Pro	Trp	Asn	Ser	Met	Ile	195	200	205	
Leu	Ile	Gly	Lys	Val	Tyr	Thr	Ala	Gln	Asn	Pro	Ser	Ala	Gln	Ala	Leu	210	215	220	
Gly	Leu	Gly	Lys	His	Asn	Tyr	Cys	Arg	Asn	Pro	Asp	Gly	Asp	Ala	Lys	225	230	235	240
Pro	Trp	Cys	His	Val	Leu	Lys	Asn	Arg	Arg	Leu	Thr	Trp	Glu	Tyr	Cys	245	250	255	
Asp	Val	Pro	Ser	Cys	Ser	Thr	Cys	Gly	Leu	Arg	Gln	Tyr	Ser	Gln	Pro	260	265	270	
Gln	Phe	Arg	Ile	Lys	Gly	Gly	Leu	Phe	Ala	Asp	Ile	Ala	Ser	His	Pro	275	280	285	
Trp	Gln	Ala	Ala	Ile	Phe	Ala	Lys	His	Arg	Arg	Ser	Pro	Gly	Glu	Arg	290	295	300	
Phe	Leu	Cys	Gly	Gly	Ile	Leu	Ile	Ser	Ser	Cys	Trp	Ile	Leu	Ser	Ala	305	310	315	320
Ala	His	Cys	Phe	Gln	Glu	Arg	Phe	Pro	Pro	His	His	Leu	Thr	Val	Ile	325	330	335	
Leu	Gly	Arg	Thr	Tyr	Arg	Val	Val	Pro	Gly	Glu	Glu	Glu	Gln	Lys	Phe	340	345	350	
Glu	Val	Glu	Lys	Tyr	Ile	Val	His	Lys	Glu	Phe	Asp	Asp	Asp	Thr	Tyr	355	360	365	
Asp	Asn	Asp	Ile	Ala	Leu	Leu	Gln	Leu	Lys	Ser	Asp	Ser	Ser	Arg	Cys	370	375	380	
Ala	Gln	Glu	Ser	Ser	Val	Val	Arg	Thr	Val	Cys	Leu	Pro	Pro	Ala	Asp	385	390	395	400
Leu	Gln	Leu	Pro	Asp	Trp	Thr	Glu	Cys	Glu	Leu	Ser	Gly	Tyr	Gly	Lys	405	410	415	
His	Glu	Ala	Leu	Ser	Pro	Phe	Tyr	Ser	Glu	Arg	Leu	Lys	Glu	Ala	His	420	425	430	

Arg Thr Val Thr Asp Asn Met Leu Cys Ala Gly Asp Thr Arg Ser Gly
450 455 460

Gly Pro Gln Ala Asn Leu His Asp Ala Cys Gln Gly Asp Ser Gly Gly
465 470 475 480

Pro Leu Val Cys Leu Asn Asp Gly Arg Met Thr Leu Val Gly Ile Ile
485 490 495

Ser Trp Gly Leu Gly Cys Gly Gln Lys Asp Val Pro Gly Val Tyr Thr
500 505 510

Lys Val Thr Asn Tyr Leu Asp Trp Ile Arg Asp Asn Met Arg Pro
515 520 525

<210> 23

<211> 211

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: SCR1-3 with an
additional 14 amino acid residues at the
C-terminus

<400> 23

Met Gln Cys Asn Ala Pro Glu Trp Leu Pro Phe Ala Arg Pro Thr Asn
1 5 10 15

Leu Thr Asp Glu Phe Glu Phe Pro Ile Gly Thr Tyr Leu Asn Tyr Glu
20 25 30

Cys Arg Pro Gly Tyr Ser Gly Arg Pro Phe Ser Ile Ile Cys Leu Lys
35 40 45

Asn Ser Val Trp Thr Gly Ala Lys Asp Arg Cys Arg Arg Lys Ser Cys
50 55 60

Arg Asn Pro Pro Asp Pro Val Asn Gly Met Val His Val Ile Lys Gly
65 70 75 80

Ile Gln Phe Gly Ser Gln Ile Lys Tyr Ser Cys Thr Lys Gly Tyr Arg
85 90 95

Leu Ile Gly Ser Ser Ser Ala Thr Cys Ile Ile Ser Gly Asp Thr Val
100 105 110

Ile Trp Asp Asn Glu Thr Pro Ile Cys Asp Arg Ile Pro Cys Gly Leu
115 120 125

Pro Pro Thr Ile Thr Asn Gly Asp Phe Ile Ser Thr Asn Arg Glu Asn
130 135 140

Phe His Tyr Gly Ser Val Val Thr Tyr Arg Cys Asn Pro Gly Ser Gly

Gly Arg Lys Val Phe Glu Leu Val Gly Glu Pro Ser Ile Tyr Cys Thr
 165 170 175

Ser Asn Asp Asp Gln Val Gly Ile Trp Ser Gly Pro Ala Pro Gln Cys
 180 185 190

Ile Ile Pro Asn Lys Asp Gly Pro Ser Glu Ile Leu Arg Gly Asp Phe
 195 200 205

Ser Ser Cys
 210

<210> 24

<211> 228

<212> PRT

<213> Artificial Sequence

<220>

<221> UNSURE

<222> (211)..(212)

<223> Residues 1-211 are a first polypeptide chain and
 residues 212-228 are a second polypeptide chain
 linked by a disulphide bond formed between the
 cysteines at positions 211 and 212

<220>

<221> UNSURE

<222> (228)

<223> The C-terminal glycine is linked to an
 -NH-[Myristoyl] group

<220>

<223> Description of Artificial Sequence: SCR1-3 with an
 additional C-terminal 14 amino acid residues
 reacted with MSWP-1

<400> 24

Met Gln Cys Asn Ala Pro Glu Trp Leu Pro Phe Ala Arg Pro Thr Asn
 1 5 10 15

Leu Thr Asp Glu Phe Glu Phe Pro Ile Gly Thr Tyr Leu Asn Tyr Glu
 20 25 30

Cys Arg Pro Gly Tyr Ser Gly Arg Pro Phe Ser Ile Ile Cys Leu Lys
 35 40 45

Asn Ser Val Trp Thr Gly Ala Lys Asp Arg Cys Arg Arg Lys Ser Cys
 50 55 60

Arg Asn Pro Pro Asp Pro Val Asn Gly Met Val His Val Ile Lys Gly
 65 70 75 80

Ile Gln Phe Gly Ser Gln Ile Lys Tyr Ser Cys Thr Lys Gly Tyr Arg
 85 90 95

Ile Trp Asp Asn Glu Thr Pro Ile Cys Asp Arg Ile Pro Cys Gly Leu
 115 120 125

Pro Pro Thr Ile Thr Asn Gly Asp Phe Ile Ser Thr Asn Arg Glu Asn
 130 135 140

Phe His Tyr Gly Ser Val Val Thr Tyr Arg Cys Asn Pro Gly Ser Gly
 145 150 155 160

Gly Arg Lys Val Phe Glu Leu Val Gly Glu Pro Ser Ile Tyr Cys Thr
 165 170 175

Ser Asn Asp Asp Gln Val Gly Ile Trp Ser Gly Pro Ala Pro Gln Cys
 180 185 190

Ile Ile Pro Asn Lys Asp Gly Pro Ser Glu Ile Leu Arg Gly Asp Phe
 195 200 205

Ser Ser Cys Cys Asp Gly Pro Lys Lys Lys Lys Lys Lys Ser Pro Ser
 210 215 220

Lys Ser Ser Gly
 225

<210> 25

<211> 72

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

Oligonucleotide used with the oligonucleotide of
 SEQ ID NO. 26 and plasmid pBC04-29 to generate
 pBC04-31

<400> 25

cgcaccgcag tgcacatcc cgaacaaaga tggcccgagc gaaattctgc gtggcgattt 60
 tagcagctgc ta 72

<210> 26

<211> 80

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

Oligonucleotide used with oligonucleotide of SEQ
 ID NO. 25 and plasmid pBC04-29 to generate plasmid
 pBC04-31

<400> 26

acgttagcag ctgctaaaat cgccacgcag aatttcgctc gggccatctt tgttcgggat 60
 gatgcactgc ggtgcgggcc 80

<212> PRT
 <213> Artificial Sequence

<220>
 <221> UNSURE
 <222> (1)
 <223> The N-terminal glycine is linked to an
 N-[Myristoyl]- group

<220>
 <223> Description of Artificial Sequence:
 Myristoyl/Electrostatic Swith Peptide Reagent 1
 (MSWP-1)

<220>
 <221> UNSURE
 <222> (17)
 <223> The cysteine at position 17 is (S-
 2-Thiopyridyl)Cys-NH2

<400> 27
 Gly Ser Ser Lys Ser Pro Ser Lys Lys Lys Lys Lys Lys Pro Gly Asp
 1 5 10 15

Cys

<210> 28
 <211> 17
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> UNSURE
 <222> (1)
 <223> The N-terminal Cys is
 N-acetyl-(S-2-thiopyridyl)Cys-

<220>
 <221> UNSURE
 <222> (17)
 <223> The C-terminal lysine is
 -(epsilonN-(Myristoyl))Lys-NH2

<220>
 <223> Description of Artificial Sequence:
 Myristoyl/Electrostatic Switch Peptide Reagent 2
 (MSWP-2)

<400> 28
 Cys Asp Gly Pro Lys Lys Lys Lys Lys Lys Ser Pro Ser Lys Ser Ser
 1 5 10 15

Lys

<210> 29
 <211> 15
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> UNSURE
 <222> (1)
 <223> The N-terminal serine is N-(Myristoyl)-Ser-

<220>
 <221> UNSURE
 <222> (15)
 <223> The C-terminal cysteine is
 - (S-2-Thiopyrolyl)Cys-NH₂

<220>
 <223> Description of Artificial Sequence:
 Myristoyl/Electrostatic Switch Peptide Reagent 3
 (MSWP-3)

<400> 29
 Ser Lys Asp Gly Lys Lys Lys Lys Lys Ser Lys Thr Lys Cys
 1 5 10 15

<210> 30
 <211> 16
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> UNSURE
 <222> (1)
 <223> The N-terminal cysteine is
 N-acetyl-(S-2-thiopyridyl)Cys-

<220>
 <221> UNSURE
 <222> (16)
 <223> The C-terminal valine is -Val-NH(CH₂)₉CH₃

<220>
 <223> Description of Artificial Sequence: T-cell
 targetting peptide reagent 1 (TCTP-1)

<400> 30
 Cys Ser Ala Ala Pro Ser Ser Gly Phe Arg Ile Leu Leu Leu Lys Val
 1 5 10 15

<210> 31
 <211> 214
 <212> PRT
 <213> Artificial Sequence

<222> (214)

<223> The C-terminal cysteine is
-Cys-S-S-(CH₂)₂-CONH-(CH₂)₁₂CH₃

<220>

<223> Description of Artificial Sequence: [SCR1-3/switch
fusion]disulphide linked to [MAET]

<400> 31

Met Gln Cys Asn Ala Pro Glu Trp Leu Pro Phe Ala Arg Pro Thr Asn
1 5 10 15

Leu Thr Asp Glu Phe Glu Phe Pro Ile Gly Thr Tyr Leu Asn Tyr Glu
20 25 30

Cys Arg Pro Gly Tyr Ser Gly Arg Pro Phe Ser Ile Ile Cys Leu Lys
35 40 45

Asn Ser Val Trp Thr Gly Ala Lys Asp Arg Cys Arg Arg Lys Ser Cys
50 55 60

Arg Asn Pro Pro Asp Pro Val Asn Gly Met Val His Val Ile Lys Gly
65 70 75 80

Ile Gln Phe Gly Ser Gln Ile Lys Tyr Ser Cys Thr Lys Gly Tyr Arg
85 90 95

Leu Ile Gly Ser Ser Ser Ala Thr Cys Ile Ile Ser Gly Asp Thr Val
100 105 110

Ile Trp Asp Asn Glu Thr Pro Ile Cys Asp Arg Ile Pro Cys Gly Leu
115 120 125

Pro Pro Thr Ile Thr Asn Gly Asp Phe Ile Ser Thr Asn Arg Glu Asn
130 135 140

Phe His Tyr Gly Ser Val Val Thr Tyr Arg Cys Asn Pro Gly Ser Gly
145 150 155 160

Gly Arg Lys Val Phe Glu Leu Val Gly Glu Pro Ser Ile Tyr Cys Thr
165 170 175

Ser Asn Asp Asp Gln Val Gly Ile Trp Ser Gly Pro Ala Pro Gln Cys
180 185 190

Ile Ile Pro Asn Lys Asp Gly Pro Lys Lys Lys Lys Lys Lys Ser Pro
195 200 205

Ser Lys Ser Ser Gly Cys
210

<210> 32

<211> 17

<212> PRT

<213> Artificial Sequence

<221> UNSURE

<222> (1)

<223> The N-terminal Glycine is N-(Myristoyl)-Gly-

<220>

<221> UNSURE

<222> (17)

<223> The C-terminal cysteine is linked to an amino group and is also linked via a disulphide bond to -[4-butyrimino]-N-epsilon(Lys)[Rabbit anti-(human erythrocyte membrane) antibody].

<220>

<223> Description of Artificial Sequence: Rabbit anti-(human erythrocyte membrane) antibody-[MSWP-1] conjugate.

<400> 32

Gly Ser Ser Lys Ser Pro Ser Lys Lys Lys Lys Lys Lys Pro Gly Asp
1 5 10 15

Cys

<210> 33

<211> 214

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: SCR1-3 with an additional C-terminal 18 amino acids

<400> 33

Met Gln Cys Asn Ala Pro Glu Trp Leu Pro Phe Ala Arg Pro Thr Asn
1 5 10 15

Leu Thr Asp Glu Phe Glu Phe Pro Ile Gly Thr Tyr Leu Asn Tyr Glu
20 25 30

Cys Arg Pro Gly Tyr Ser Gly Arg Pro Phe Ser Ile Ile Cys Leu Lys
35 40 45

Asn Ser Val Trp Thr Gly Ala Lys Asp Arg Cys Arg Arg Lys Ser Cys
50 55 60

Arg Asn Pro Pro Asp Pro Val Asn Gly Met Val His Val Ile Lys Gly
65 70 75 80

Ile Gln Phe Gly Ser Gln Ile Lys Tyr Ser Cys Thr Lys Gly Tyr Arg
85 90 95

Leu Ile Gly Ser Ser Ser Ala Thr Cys Ile Ile Ser Gly Asp Thr Val
100 105 110

Pro Pro Thr Ile Thr Asn Gly Asp Phe Ile Ser Thr Asn Arg Glu Asn
 130 135 140

Phe His Tyr Gly Ser Val Val Thr Tyr Arg Cys Asn Pro Gly Ser Gly
 145 150 155 160

Gly Arg Lys Val Phe Glu Leu Val Gly Glu Pro Ser Ile Tyr Cys Thr
 165 170 175

Ser Asn Asp Asp Gln Val Gly Ile Trp Ser Gly Pro Ala Pro Gln Cys
 180 185 190

Ile Ile Pro Asn Lys Ala Ala Pro Ser Val Ile Gly Phe Arg Ile Leu
 195 200 205

Leu Leu Lys Val Gly Cys
 210

<210> 34
 <211> 84
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:
 Oligonucleotide used with oligonucleotide of SEQ
 ID NO.35 and plasmid pBC04-29 to generate plasmid
 pBC04-34

<400> 34
 cgcaccgcag tgcacatcc cgaacaaagc ggcgcccagc gtgattggct tccgtattct 60
 gctgctgaaa gtggcgggct gcta 84

<210> 35
 <211> 92
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:
 Oligonucleotide used with the oligonucleotide of
 SEQ ID NO. 34 and plasmid pBC04-29 to generate
 plasmid pBC04-34

<400> 35
 agcttagcag cccgccactt tcagcagcag aatacggag ccaatcacgc tgggcgccgc 60
 ttgttcggg atgatgcact gcggtgcggg cc 92

<210> 36
 <211> 231
 <212> PRT
 <213> Artificial Sequence

<223> Residues 1-214 are a first polypeptide chain and residues 215-231 are a second polypeptide chain linked by a disulphide bond formed between the cysteines at positions 214 and 215

<220>

<221> UNSURE

<222> (231)

<223> The C-terminal glycine is -Gly-NH-[Myristoyl]

<220>

<223> Description of Artificial Sequence: [SCR1-3] with an additional 18 C-terminal amino acid residues linked via a disulphide bond to MSWP-1

<400> 36

Met	Gln	Cys	Asn	Ala	Pro	Glu	Trp	Leu	Pro	Phe	Ala	Arg	Pro	Thr	Asn
1				5					10					15	

Leu	Thr	Asp	Glu	Phe	Glu	Phe	Pro	Ile	Gly	Thr	Tyr	Leu	Asn	Tyr	Glu
			20					25					30		

Cys	Arg	Pro	Gly	Tyr	Ser	Gly	Arg	Pro	Phe	Ser	Ile	Ile	Cys	Leu	Lys
		35					40					45			

Asn	Ser	Val	Trp	Thr	Gly	Ala	Lys	Asp	Arg	Cys	Arg	Arg	Lys	Ser	Cys
	50					55					60				

Arg	Asn	Pro	Pro	Asp	Pro	Val	Asn	Gly	Met	Val	His	Val	Ile	Lys	Gly
65					70				75						80

Ile	Gln	Phe	Gly	Ser	Gln	Ile	Lys	Tyr	Ser	Cys	Thr	Lys	Gly	Tyr	Arg
			85						90					95	

Leu	Ile	Gly	Ser	Ser	Ser	Ala	Thr	Cys	Ile	Ile	Ser	Gly	Asp	Thr	Val
		100						105					110		

Ile	Trp	Asp	Asn	Glu	Thr	Pro	Ile	Cys	Asp	Arg	Ile	Pro	Cys	Gly	Leu
		115					120					125			

Pro	Pro	Thr	Ile	Thr	Asn	Gly	Asp	Phe	Ile	Ser	Thr	Asn	Arg	Glu	Asn
	130					135					140				

Phe	His	Tyr	Gly	Ser	Val	Val	Thr	Tyr	Arg	Cys	Asn	Pro	Gly	Ser	Gly
145					150					155					160

Gly	Arg	Lys	Val	Phe	Glu	Leu	Val	Gly	Glu	Pro	Ser	Ile	Tyr	Cys	Thr
			165					170						175	

Ser	Asn	Asp	Asp	Gln	Val	Gly	Ile	Trp	Ser	Gly	Pro	Ala	Pro	Gln	Cys
		180						185					190		

Ile	Ile	Pro	Asn	Lys	Ala	Ala	Pro	Ser	Val	Ile	Gly	Phe	Arg	Ile	Leu
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Ser Pro Ser Lys Ser Ser Gly
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<220>
 <223> Description of Artificial Sequence: illustrative amino
 acid sequence

<400> 37
 Asp Gly Pro Lys Lys Lys Lys Lys Lys Ser Pro Ser Lys Ser Ser Gly
 1 5 10 15

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<220>
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Lys Lys Ser Gly
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<223> Description of Artificial Sequence: illustrative amino acid sequence

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<223> Description of Artificial Sequence: illustrative amino

Gly Asn Glu Gln Ser Phe Arg Val Asp Leu Arg Thr Leu Leu Arg Tyr
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<223> Description of Artificial Sequence: illustrative amino acid sequence

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Gly Phe Arg Ile Leu Leu Leu Lys Val
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<223> Description of Artificial Sequence: illustrative amino acid sequence

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Gly

<210> 48

<211> 17

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Asp Gly Pro Lys Lys Lys Lys Lys Lys Ser Pro Ser Lys Ser Ser Gly
 1 5 10 15

Cys

<210> 49

<211> 18

<212> PRT

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<400> 49

Ala Ala Pro Ser Val Ile Gly Phe Arg Ile Leu Leu Leu Lys Val Ala
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Gly Cys

<210> 50

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<212> PRT

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<400> 50

Asp Gly Pro Ser Glu Ile Leu Arg Gly Asp Phe Ser Ser Cys
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